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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/021,571

DATE: 12/31/2001

TIME: 12:55:43

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\12312001\J021571.raw

ENTERED

3 <110> APPLICANT: CHAO, Moses V.
 4 KONG, Haeyoung
 6 <120> TITLE OF INVENTION: A TRANSMEMBRANE PROTEIN AS A DOWNSTREAM TARGET OF
 NEUROTROPHIN AND EPHRIN
 7 RECEPTOR TYROSINE KINASES, DNA ENCODING SAME AND MONOCLONAL ANTIBODIES THERETO
 9 <130> FILE REFERENCE: CHAO11A
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/021,571
 12 <141> CURRENT FILING DATE: 2001-12-19
 14 <150> PRIOR APPLICATION NUMBER: 60/256,909
 15 <151> PRIOR FILING DATE: 2000-12-21
 17 <160> NUMBER OF SEQ ID NOS: 8
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 5148
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Rattus norvegicus
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (1)..(5148)
 29 <223> OTHER INFORMATION:
 32 <400> SEQUENCE: 1
 33 atg tca gtt ctt ata tca cag agt gtg ata aat tat gtg gaa gaa gag 48
 34 Met Ser Val Leu Ile Ser Gln Ser Val Ile Asn Tyr Val Glu Glu Glu
 35 1 5 10 15
 37 aat att cct gct ctg aaa gct ctt ctt gag aag tgc aaa gat gta gat 96
 38 Asn Ile Pro Ala Leu Lys Ala Leu Leu Glu Lys Cys Lys Asp Val Asp
 39 20 25 30
 41 gag agg aac gag tgt ggc cag acg ccg ctg atg ctg gct gcg gag cag 144
 42 Glu Arg Asn Glu Cys Gly Gln Thr Pro Leu Met Leu Ala Ala Glu Gln
 43 35 40 45
 45 ggc aat gtg gaa ata gtg aaa gaa ctg tta aag aat gga gcc aac tgc 192
 46 Gly Asn Val Glu Ile Val Lys Glu Leu Leu Lys Asn Gly Ala Asn Cys
 47 50 55 60
 49 aat ctg gaa gat ctg gat aac tgg act gcc ctt ata tcg gca tct aag 240
 50 Asn Leu Glu Asp Leu Asp Asn Trp Thr Ala Leu Ile Ser Ala Ser Lys
 51 65 70 75 80
 53 gag ggg cac atc cac att gtg gag gag ctg ctg aag agc ggg gcc agt 288
 54 Glu Gly His Ile His Ile Val Glu Glu Leu Leu Lys Ser Gly Ala Ser
 55 85 90 95
 57 ctg gag cac cga gac atg ggt gga tgg aca gct ctc atg tgg gcg tgc 336
 58 Leu Glu His Arg Asp Met Gly Gly Trp Thr Ala Leu Met Trp Ala Cys
 59 100 105 110
 61 tac aaa ggc agg acc gac gtg gtc gag ctg ctt ctt tct cat ggt gcc 384
 62 Tyr Lys Gly Arg Thr Asp Val Val Glu Leu Leu Leu Ser His Gly Ala
 63 115 120 125
 65 aac cca agt gtc act ggt ttg cag tat agt gtc tac cca atc atc tgg 432
 66 Asn Pro Ser Val Thr Gly Leu Gln Tyr Ser Val Tyr Pro Ile Ile Trp
 67 130 135 140

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70	Ala Ala Gly Arg Gly His Ala Asp Ile Val His Leu Leu Leu Gln Asn	
71	145 150 155 160	
73	ggt gcg aaa gtc aat tgc tcc gac aag tac gga aca acc ccc ttg gta	528
74	Gly Ala Lys Val Asn Cys Ser Asp Lys Tyr Gly Thr Thr Pro Leu Val	
75	165 170 175	
77	tgg gct gcc cga aag ggt cat ttg gaa tgt gtg aag cac ttg ttg gcc	576
78	Trp Ala Ala Arg Lys Gly His Leu Glu Cys Val Lys His Leu Leu Ala	
79	180 185 190	
81	atg gga gct gat gtt gat caa gaa gga gcc aat tcg atg act gca ctt	624
82	Met Gly Ala Asp Val Asp Gln Glu Gly Ala Asn Ser Met Thr Ala Leu	
83	195 200 205	
85	atc gtg gca gtg aaa gga ggc tac aca cag tcc gtg aaa gag att ttg	672
86	Ile Val Ala Val Lys Gly Gly Tyr Thr Gln Ser Val Lys Glu Ile Leu	
87	210 215 220	
89	aaa agg aat cca aat gtg aac cta act gac aag gat gga aac aca gct	720
90	Lys Arg Asn Pro Asn Val Asn Leu Thr Asp Lys Asp Gly Asn Thr Ala	
91	225 230 235 240	
93	ctg atg atc gca tcg aag gag gga cat att gag att gtg cag gac ctg	768
94	Leu Met Ile Ala Ser Lys Glu Gly His Ile Glu Ile Val Gln Asp Leu	
95	245 250 255	
97	ctg gac gcc gga aca tac gtg aac ata cct gac agg agt ggg gat act	816
98	Leu Asp Ala Gly Thr Tyr Val Asn Ile Pro Asp Arg Ser Gly Asp Thr	
99	260 265 270	
101	gta ttg atc ggc gct gtg aga ggt ggt cat gtt gaa att gtt cga gca	864
102	Val Leu Ile Gly Ala Val Arg Gly Gly His Val Glu Ile Val Arg Ala	
103	275 280 285	
105	ctt ctc caa aaa tat gct gat ata gac att aga ggg cag gac aat aag	912
106	Leu Leu Gln Lys Tyr Ala Asp Ile Asp Ile Arg Gly Gln Asp Asn Lys	
107	290 295 300	
109	acc gcg ctg tat tgg gcc gtt gaa aag gga aat gcg aca atg gtg agg	960
110	Thr Ala Leu Tyr Trp Ala Val Glu Lys Gly Asn Ala Thr Met Val Arg	
111	305 310 315 320	
113	gat atc ctg cag tgc aat ccg gac acg gaa ata tgc acg aag gat ggt	1008
114	Asp Ile Leu Gln Cys Asn Pro Asp Thr Glu Ile Cys Thr Lys Asp Gly	
115	325 330 335	
117	gag aca cca ctg ata aaa gcc acc aag atg aga aat att gaa gtg gtg	1056
118	Glu Thr Pro Leu Ile Lys Ala Thr Lys Met Arg Asn Ile Glu Val Val	
119	340 345 350	
121	gag ctg ctg ctg gat aag ggg gct aag gtg tct gct gtg gac aag aaa	1104
122	Glu Leu Leu Leu Asp Lys Gly Ala Lys Val Ser Ala Val Asp Lys Lys	
123	355 360 365	
125	ggg gac act ccc ctg cac gtt gcc atc cga ggg agg agc cgg aga ctg	1152
126	Gly Asp Thr Pro Leu His Val Ala Ile Arg Gly Arg Ser Arg Arg Leu	
127	370 375 380	
129	gcc gaa ctt ctt tta cgg aac ccc aaa gat gga cgg tta ctc tac aga	1200
130	Ala Glu Leu Leu Leu Arg Asn Pro Lys Asp Gly Arg Leu Leu Tyr Arg	
131	385 390 395 400	
133	ccc aac aaa gca ggc gag act ccc tac aac att gac tgc agc cac cag	1248

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134	Pro	Asn	Lys	Ala	Gly	Glu	Thr	Pro	Tyr	Asn	Ile	Asp	Cys	Ser	His	Gln	
135					405					410					415		
137	aaa	agc	att	tta	act	caa	ata	ttt	gga	gcc	aga	cac	ttg	tct	cct	acg	1296
138	Lys	Ser	Ile	Leu	Thr	Gln	Ile	Phe	Gly	Ala	Arg	His	Leu	Ser	Pro	Thr	
139				420					425					430			
141	gaa	aca	gat	ggc	gac	atg	ctt	ggt	tat	gat	ttg	tat	agc	agt	gcc	ctg	1344
142	Glu	Thr	Asp	Gly	Asp	Met	Leu	Gly	Tyr	Asp	Leu	Tyr	Ser	Ser	Ala	Leu	
143			435					440					445				
145	gcc	gat	att	ctc	agt	gaa	ccc	acc	atg	caa	cca	ccc	att	tgt	gtg	ggc	1392
146	Ala	Asp	Ile	Leu	Ser	Glu	Pro	Thr	Met	Gln	Pro	Pro	Ile	Cys	Val	Gly	
147		450					455					460					
149	ttg	tat	gca	cag	tgg	gga	agt	ggg	aag	tct	ttc	tta	ctc	aag	aaa	cta	1440
150	Leu	Tyr	Ala	Gln	Trp	Gly	Ser	Gly	Lys	Ser	Phe	Leu	Leu	Lys	Lys	Leu	
151	465				470				475						480		
153	gaa	gat	gag	atg	aag	acg	ttt	gca	gga	cag	cag	acc	gag	ccc	ctc	ttc	1488
154	Glu	Asp	Glu	Met	Lys	Thr	Phe	Ala	Gly	Gln	Gln	Thr	Glu	Pro	Leu	Phe	
155				485					490					495			
157	cag	ttc	tcg	tgg	ctc	ata	gtg	ttc	ctc	acc	ctg	ctg	ctg	tgt	ggc	ggg	1536
158	Gln	Phe	Ser	Trp	Leu	Ile	Val	Phe	Leu	Thr	Leu	Leu	Leu	Cys	Gly	Gly	
159			500					505					510				
161	ctc	ggc	cta	gtg	ttt	gct	ttc	ccg	gtt	gat	aca	aac	ctc	gcc	ata	gcc	1584
162	Leu	Gly	Leu	Val	Phe	Ala	Phe	Pro	Val	Asp	Thr	Asn	Leu	Ala	Ile	Ala	
163		515						520				525					
165	att	tca	ttg	agt	ttc	ctg	gct	ctc	ata	tat	ata	ttc	ttc	atc	gtc	att	1632
166	Ile	Ser	Leu	Ser	Phe	Leu	Ala	Leu	Ile	Tyr	Ile	Phe	Phe	Ile	Val	Ile	
167		530				535					540						
169	tac	ttc	ggt	gga	cgg	cgg	gaa	gga	gag	agt	tgg	aac	tgg	gcc	tgg	gct	1680
170	Tyr	Phe	Gly	Gly	Arg	Arg	Glu	Gly	Glu	Ser	Trp	Asn	Trp	Ala	Trp	Ala	
171	545				550				555					560			
173	ctc	agt	acc	aga	ctg	gca	aga	cac	att	ggg	tac	ctg	gag	ctc	ctc	ttc	1728
174	Leu	Ser	Thr	Arg	Leu	Ala	Arg	His	Ile	Gly	Tyr	Leu	Glu	Leu	Leu	Phe	
175				565					570					575			
177	aaa	ctg	atg	ttt	gtg	aac	cca	cct	gaa	ctg	ccg	gag	caa	act	aca	aag	1776
178	Lys	Leu	Met	Phe	Val	Asn	Pro	Pro	Glu	Leu	Pro	Glu	Gln	Thr	Thr	Lys	
179			580					585					590				
181	gct	tta	cct	gtg	agg	ttt	ttg	ttt	aca	gat	tac	aat	aga	ctc	tcc	agt	1824
182	Ala	Leu	Pro	Val	Arg	Phe	Leu	Phe	Thr	Asp	Tyr	Asn	Arg	Leu	Ser	Ser	
183		595					600					605					
185	gtg	gga	gga	gaa	act	tcc	ttg	gct	gaa	atg	atc	gcg	acc	ctc	tca	gat	1872
186	Val	Gly	Gly	Glu	Thr	Ser	Leu	Ala	Glu	Met	Ile	Ala	Thr	Leu	Ser	Asp	
187		610					615					620					
189	gct	tgt	gag	aga	gaa	ttc	ggc	ttt	ttg	gct	acc	cgt	ctt	ttt	cga	gtc	1920
190	Ala	Cys	Glu	Arg	Glu	Phe	Gly	Phe	Leu	Ala	Thr	Arg	Leu	Phe	Arg	Val	
191	625				630				635					640			
193	ttc	agg	act	gaa	gag	tct	cag	ggt	aaa	aag	aaa	tgg	aaa	aaa	aca	tgc	1968
194	Phe	Arg	Thr	Glu	Glu	Ser	Gln	Gly	Lys	Lys	Lys	Trp	Lys	Lys	Thr	Cys	
195				645				650						655			
197	tgc	ctc	ccc	tct	ttt	gtc	atc	ttt	ctt	ttt	att	gtt	ggc	tgc	att	att	2016
198	Cys	Leu	Pro	Ser	Phe	Val	Ile	Phe	Leu	Phe	Ile	Val	Gly	Cys	Ile	Ile	

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199		660		665		670		
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202	Ala Gly Ile Thr Leu Leu Ala Ile Phe Arg Val Asp Pro Lys His Leu							
203		675		680		685		
205	aca gtg aat gct atc ctc att tct atc gca tct gtc gtg ggg ttg gcc							2112
206	Thr Val Asn Ala Ile Leu Ile Ser Ile Ala Ser Val Val Gly Leu Ala							
207		690		695		700		
209	ttc gtg ctc aat tgt cga aca tgg tgg caa gtg ctg gac tct ctc ctg							2160
210	Phe Val Leu Asn Cys Arg Thr Trp Trp Gln Val Leu Asp Ser Leu Leu							
211	705		710		715		720	
213	aat tct cag aga aaa cgc ctc cat agt gct gcc tcc aaa tta cac aag							2208
214	Asn Ser Gln Arg Lys Arg Leu His Ser Ala Ala Ser Lys Leu His Lys							
215		725		730		735		
217	tta aaa agt gaa gga ttc atg aaa gtc ctg aag tgt gag gtg gag ctg							2256
218	Leu Lys Ser Glu Gly Phe Met Lys Val Leu Lys Cys Glu Val Glu Leu							
219		740		745		750		
221	atg gcc agg atg gca aaa acc att gac agc ttc act caa aac cag aca							2304
222	Met Ala Arg Met Ala Lys Thr Ile Asp Ser Phe Thr Gln Asn Gln Thr							
223		755		760		765		
225	agg ctg gtg gtt atc att gac ggc ctg gat gcc tgc gag cag gat aaa							2352
226	Arg Leu Val Val Ile Ile Asp Gly Leu Asp Ala Cys Glu Gln Asp Lys							
227		770		775		780		
229	gtc ctt cag atg ctg gac act gtc cga gtt ctg ttt tca aag ggc cct							2400
230	Val Leu Gln Met Leu Asp Thr Val Arg Val Leu Phe Ser Lys Gly Pro							
231	785		790		795		800	
233	ttt att gcc att ttt gca agt gat ccg cat att atc ata aag gcc atc							2448
234	Phe Ile Ala Ile Phe Ala Ser Asp Pro His Ile Ile Ile Lys Ala Ile							
235		805		810		815		
237	aac cag aac ctg aat agt gtg ctt cgt gac tca aat ata aac gga cat							2496
238	Asn Gln Asn Leu Asn Ser Val Leu Arg Asp Ser Asn Ile Asn Gly His							
239		820		825		830		
241	gac tac atg cgc aat ata gtt cac tta cca gtt ttt ctt aat agt cgt							2544
242	Asp Tyr Met Arg Asn Ile Val His Leu Pro Val Phe Leu Asn Ser Arg							
243		835		840		845		
245	ggg ctt agc aat gca agg aaa ttc ctt gta act tca gca aca aat ggg							2592
246	Gly Leu Ser Asn Ala Arg Lys Phe Leu Val Thr Ser Ala Thr Asn Gly							
247		850		855		860		
249	gac att aca tgc tca gac acc aca gga aca cag gag gac act gac aga							2640
250	Asp Ile Thr Cys Ser Asp Thr Thr Gly Thr Gln Glu Asp Thr Asp Arg							
251	865		870		875		880	
253	aga gtt tca cag aac agc ctt ggg gag atg aca aag ctt ggg agc aaa							2688
254	Arg Val Ser Gln Asn Ser Leu Gly Glu Met Thr Lys Leu Gly Ser Lys							
255		885		890		895		
257	acg gct ctc aac aga agg gac act tac cgc aga aga cag atg cag aga							2736
258	Thr Ala Leu Asn Arg Arg Asp Thr Tyr Arg Arg Arg Gln Met Gln Arg							
259		900		905		910		
261	acc atc acg agg cag atg tcc ttt gat ctc aca aag ctg ctg gtc act							2784
262	Thr Ile Thr Arg Gln Met Ser Phe Asp Leu Thr Lys Leu Leu Val Thr							
263		915		920		925		

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265	gag	gat	tgg	ttc	agt	gac	atc	agc	cct	cag	acc	atg	aga	cgg	cta	ctc	2832
266	Glu	Asp	Trp	Phe	Ser	Asp	Ile	Ser	Pro	Gln	Thr	Met	Arg	Arg	Leu	Leu	
267		930					935					940					
269	aat	att	gtt	tct	gtg	aca	ggg	cgg	cta	cta	aga	gcc	aat	cag	att	act	2880
270	Asn	Ile	Val	Ser	Val	Thr	Gly	Arg	Leu	Leu	Arg	Ala	Asn	Gln	Ile	Thr	
271	945					950					955				960		
273	ttc	aac	tgg	gac	agg	cta	gcc	agc	tgg	atc	aac	ctc	acc	gag	cag	tgg	2928
274	Phe	Asn	Trp	Asp	Arg	Leu	Ala	Ser	Trp	Ile	Asn	Leu	Thr	Glu	Gln	Trp	
275				965					970					975			
277	ccg	tac	cgg	acg	tct	tgg	ctt	ata	cta	tat	ctg	gaa	gag	act	gaa	ggt	2976
278	Pro	Tyr	Arg	Thr	Ser	Trp	Leu	Ile	Leu	Tyr	Leu	Glu	Glu	Thr	Glu	Gly	
279				980				985				990					
281	ctc	cct	gat	cag	atg	acc	tta	aag	acc	atg	tat	gag	aga	ata	tcg	aag	3024
282	Leu	Pro	Asp	Gln	Met	Thr	Leu	Lys	Thr	Met	Tyr	Glu	Arg	Ile	Ser	Lys	
283			995				1000					1005					
285	aat	atc	cca	aca	act	aaa	gat	gtt	gag	ccg	ctt	ctt	gaa	att	gat		3069
286	Asn	Ile	Pro	Thr	Thr	Lys	Asp	Val	Glu	Pro	Leu	Leu	Glu	Ile	Asp		
287		1010					1015					1020					
289	gga	gat	ata	aga	aac	ttt	gaa	gtc	ttc	ttg	tct	tca	agg	act	cca		3114
290	Gly	Asp	Ile	Arg	Asn	Phe	Glu	Val	Phe	Leu	Ser	Ser	Arg	Thr	Pro		
291		1025					1030					1035					
293	gtt	ctc	gtg	gct	cga	gat	gta	aag	acc	ttt	ttg	ccg	tgc	aca	gta		3159
294	Val	Leu	Val	Ala	Arg	Asp	Val	Lys	Thr	Phe	Leu	Pro	Cys	Thr	Val		
295		1040					1045					1050					
297	aac	ctg	gat	ccc	aaa	ctt	cgg	gag	atc	atc	gca	gat	gtc	cga	gct		3204
298	Asn	Leu	Asp	Pro	Lys	Leu	Arg	Glu	Ile	Ile	Ala	Asp	Val	Arg	Ala		
299		1055					1060					1065					
301	gca	aga	gag	cag	atc	aac	ata	gga	ggc	ctg	gcc	tat	ccc	ccg	ctc		3249
302	Ala	Arg	Glu	Gln	Ile	Asn	Ile	Gly	Gly	Leu	Ala	Tyr	Pro	Pro	Leu		
303		1070					1075					1080					
305	cct	ctg	cac	gaa	ggc	cct	cct	cgg	cca	cct	tct	ggg	tac	agt	cag		3294
306	Pro	Leu	His	Glu	Gly	Pro	Pro	Arg	Pro	Pro	Ser	Gly	Tyr	Ser	Gln		
307		1085					1090					1095					
309	cct	gca	tct	gtc	tgc	tct	tca	gca	tct	ttc	aac	ggg	ccg	ttc	cca		3339
310	Pro	Ala	Ser	Val	Cys	Ser	Ser	Ala	Ser	Phe	Asn	Gly	Pro	Phe	Pro		
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314	Gly	Gly	Val	Val	Ser	Pro	Gln	Pro	His	Ser	Ser	Tyr	Tyr	Ser	Gly		
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317	ttg	tcc	gga	ccc	cag	cac	ccc	ttc	tac	aac	agg	gca	gcc	gtc	cct		3429
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322	Ala	Thr	Gly	Ser	Ser	Leu	Leu	Leu	Ser	Ser	Met	Thr	Val	Asp	Val		
323		1145					1150					1155					
325	gta	tgt	gag	aaa	ctg	aga	cag	ata	gaa	ggg	ctg	gac	cag	aac	atg		3519
326	Val	Cys	Glu	Lys	Leu	Arg	Gln	Ile	Glu	Gly	Leu	Asp	Gln	Asn	Met		
327		1160					1165					1170					
329	atg	cct	cag	tac	tgc	aca	aca	atc	aaa	aag	gcg	aac	ata	aat	ggc		3564

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number